Top-k Utility-based Gene Regulation Sequential Pattern Discovery

Morteza Zihayat, Heidar Davoudi, Aijun An
Department of Electrical Engineering and Computer Science
York University, Toronto, Ontario, Canada
Email: {zihayatm,davoudi,aan}@cse.yorku.ca

***Abstract*—Sequential pattern mining has been used in bioinformatics to discover frequent gene regulation sequential patterns based on time course microarray datasets. While mining frequent sequences are important in biological studies for disease treatment, to date, most of the approaches do not consider the importance of the genes with respect to a disease being studied when identifying gene regulation sequential patterns. In addition, they focus on the more general up/down effects of genes in a microarray dataset and do not take into account the various degrees of expression during the mining process. As a result, the current techniques return too many sequences which may not be informative enough for biologists to explore relationships between the disease and underlying causes encoded in gene regulation sequences. In this paper, we propose a *utility* model by considering both the *importance of genes* with respect to a disease and their *degrees of expression levels* under a biological investigation. Then, we design a new method, called *TU-SEQ*, for identifying *top-k high utility gene regulation sequential patterns* from a time-course microarray dataset. The evaluation results show that our approach can effectively and efficiently discover key patterns representing meaningful gene regulation sequential patterns in a time course microarray dataset.**

I. Introduction

Microarrays have been widely used in the biomedical field for discovering differentially expressed genes in human diseases. Many methods have been proposed to monitor massive gene expressions and identify their regulations during a clinical study. However, more and more evidence shows that a human disease cannot be attributed to a single gene but emerges as complex interactions among multiple genetic variants [1]. In recent years, time course gene regulation sequential pattern analysis has become critical in illness events such as cancer formation. Such diseases have to be studied and monitored for a period of time to identify abnormal alternations in gene expressions. However, most of the existing approaches focus on how to discover differentially expressed genes varied with time and they do not consider the associations among these genes. Recently, some studies such as [1], [2], [3], [4] propose to use *sequential pattern mining* approaches to discover gene regulation sequential patterns.

Sequential pattern mining is an important task in data mining and has been extensively studied by many researchers [5]. Given a dataset of sequences, each containing a list of items/itemsets, sequential pattern mining is to discover sequences of items/itemsets that frequently appear in the dataset. If a potential gene regulation sequential pattern occurs frequently in a period of time in a gene expression dataset, it can be discovered by mining sequential patterns from the dataset.

Although sequential pattern mining has been used to discover gene regulation sequential patterns, some major limitations exist in the previous algorithms. First, these methods mostly choose important sequences based on the *frequency/support* framework. That is, only gene regulation sequences whose frequency is no less than a user-defined support threshold are chosen as interesting/important gene regulation sequential patterns. However, as clinical studies have shown, the frequency alone may not be informative enough to discover sequences regarding a specific disease. For example, some genes are more important than others in causing a particular disease and some genes are more effective than others in fighting diseases. Moreover, most of the existing approaches consider the more general up/down effects of gene's behavior (i.e., gene expression) in a microarray dataset by binning the expression value as *highly expressed* or *highly repressed* and do not take into account the degree of expressions. For example, a gene may not occur frequently but its behavior is highly remarkable in each appearance or vice versa. As a result, sequences that contain highly important or highly expressed/repressed genes may not be discovered by the frequency-based approaches because they neither consider the importance of genes, nor the various degrees of expression under a biological investigation. To address these limitations of frequency-based mining approaches, a *utility* is introduced to perform sequential pattern mining. *High utility sequential pattern (HUSP)* mining aims at extracting valuable and useful sequential patterns from data with respect to an objective. A sequence is a *high utility sequential pattern*, if its utility, defined based on the objective, in a dataset is no less than a *minimum utility threshold*. Nonetheless, existing *HUSP* mining methods are mainly applied to discovering patterns in market basket analysis (e.g., finding profitable customer shopping behavior), and have not been used to find patterns from complex sequential datasets such as time course microarray datasets. In addition, how to define the utility so that it reflects the objective (e.g., a specific disease) effectively and how to convert input sequential dataset (e.g., a time course microarray dataset) to a utility-based sequential database are challenging problems. Second, in gene regulation sequential pattern discovery, it is hard for biologists to determine the

978-1-5090-1610-5/16/$31.00 ©2016 IEEE

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.

value for the threshold. If the threshold is set too low, a large number of patterns can be found, which is not only time and memory consuming but also makes it hard to analyze the mining results. On the other hand, if the threshold is set too high, there may be very few or even no patterns being found, which means that some interesting patterns are missed. In practice, it is more interesting for biologists to set a bound on the size of output (e.g., top-k patterns), instead of giving a fixed threshold. However, since the threshold is not given in top-k pattern mining, the algorithm essentially needs to start searching for patterns with a very low threshold (e.g., zero or a value close to zero) in order to guarantee that at least k patterns can be found. This incurs very high computational costs. A main challenge is how to increase the threshold without missing any top-k patterns.

To address the above issues, we propose a new algorithm called *TU-SEQ (Top-k Utility-based gene regulation SEQuential pattern discovery)* to mine top-k high utility gene regulation sequential patterns (to be defined later) by considering the *gene importance* and their *degrees of expression* under a biological investigation. The proposed method only requires specifying a user-desired number k and a disease (as the objective) to explore the k most important gene regulation sequential patterns from a time course microarray dataset. *TU-SEQ* guarantees that no top-k high utility gene regulation sequences, which take place across different time points during the course of biological observations, will be missed. To the best of our knowledge, our work is the first step towards exploring the impact of both the *gene importance* and their *finer degrees of expression levels* under a biological investigation to discover gene regulation sequential patterns. We are hoping this research can shed a light for further research on discovering meaningful patterns from time course microarray datasets. Our contributions are summarized as follows.

- We formulate the problem of *top-k utility-based gene regulation sequential pattern discovery*. In this regard, we define a utility model by considering both the *importance of genes* with respect to a disease and their *finer degrees of expression* under a biological investigation.
- We propose an efficient algorithm, called *TU-SEQ*, for mining top-k high utility gene regulation sequences from a time course microarray dataset.
- We propose several strategies for initializing and dynamically adjusting the threshold before and during the mining process. The proposed strategies will not miss any top-k patterns.
- We conduct experiments on a real and publicly available time course microarray dataset to evaluate the effectiveness and efficiency of *TU-SEQ*.
- We develop a web interface[1] to our system. To the best of our knowledge, this is the first demonstration for top-k utility-based gene regulation sequence discovery.

The rest of the paper is organized as follows. Section II summarizes the related work. Section III presents preliminaries and the problem statement. The proposed method is discussed in Section IV. We report our experimental results in Section V. Finally, Section VI concludes the paper.

[1]Demo available at http://graph.cse.yorku.ca:8080/GeneAssociation/

II. Related Work

Sequential pattern mining has been widely used in the bioinformatics domain for discovering rules for organization of certain elements in genes, for predicting protein function, for analyzing gene expression, for motif discovery in DNA sequences and for discovering sets of genes that are frequently co-expressed in most biological conditions in a microarray dataset. Some of these methods are *apriori algorithm* [6], *half-spaces* [4], and *FPtree algorithm* [7]. Moreover, in [8], a method, called *MAGIIC*, is proposed to discover the structure motifs from protein sequences. In [2], the authors propose an algorithm called *CTGR-Span (Cross-Timepoint Gene Regulation Sequential pattern)* to efficiently discover *CTGR-SPs (Cross-Timepoint Gene Regulation Sequential Patterns)*. However, to the best of our knowledge, all of the aforementioned methods do not consider the objective of the study. That is, the temporal behavior of genes under a biological investigation is ignored in the problem setting, so is the importance of genes with respect to a disease.

Many studies have been also conducted to analyze the association between genes and a specific disease [1]. However, such methods only consider the behavior of each gene individually and they do not take the sequential relationships among genes into account. In [3], the authors propose a method to discover novelty in sequential patterns with respect to a disease (e.g., Alzheimer). However, they do not consider time course sequential databases and also the proposed method still discovers pattern based on frequency.

High utility sequential pattern (HUSP) mining has been studied recently [9], [10], [11], [12], [13], [14]. The concept of HUSP mining was first proposed by Ahmed et al [9]. They proposed two algorithms, called UL and US, for mining HUSPs. UL is a level-wise candidate generation-and-testing algorithm and US is a pattern growth method inspired by PrefixSpan [15]. Yin et al. [12] proposed the USpan algorithm for mining HUSPs. In this study, a lexicographic tree was used to extract the complete set of high utility sequential patterns and designed mechanisms for expanding the tree with two pruning strategies. In [14], we proposed a single-pass algorithm to find high utility sequential patterns in a dynamic data stream environment. We also showed that *HUSP-Stream* outperforms USpan in terms of run time and memory usage. However, most of the mentioned methods do not find patterns from complex sequential datasets such as time course microarray datasets.

So far, no study has been conducted to learn *utility-based gene regulation sequential patterns* in a time course microarray dataset, which is more challenging than finding frequent time course gene regulation sequential patterns.

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.

TABLE I
(A) AN EXAMPLE OF A TIME COURSE MICROARRAY DATASET, (B) FOLD CHANGES OF GENE/PROBE VALUES

Patient IDs	*Genes*	TS_1	TS_2	TS_3	TS_4
P_1	G_1	240	546	100	50
	G_2	321	98	454	974
	G_3	410	350	251	243
P_2	G_1	128	786	135	344
	G_2	253	820	482	90
	G_3	290	150	256	864
P_3	G_1	600	188	99	40
	G_2	500	555	510	80
	G_3	200	400	350	450

(a)

Patient IDs	*Genes*	TS_1	TS_2	TS_3	TS_4
P_1	G_1	1	2.2	−2.4	−4.8
	G_2	1	−3.2	1.4	3.0
	G_3	1	−1.1	−1.6	−1.6
P_2	G_1	1	6.1	1.0	2.6
	G_2	1	3.2	1.9	−2.8
	G_3	1	−1.9	−1.1	2.9
P_3	G_1	1	−3.1	−6.6	−15
	G_2	1	1.1	1.0	−6.2
	G_3	1	2	1.7	2.2

(b)

TABLE II
(A) A TIME COURSE SEQUENTIAL DATASET FROM TIME COURSE MICROARRAY DATASET IN TABLE I(A), (B) GENE IMPORTANCE TABLE

Patient IDs	*Sequence*
P_1	$\{G_{1^+}(2.2)G_{2^-}(3.2)\}_2\ \{G_{1^-}(2.4)G_{3^-}(1.6)\}_3\{G_{1^-}(4.8)G_{2^+}(3.0)G_{3^-}(1.6)\}_4$
P_2	$\{G_{1^+}(6.1)G_{2^+}(3.2)G_{3^-}(1.9)\}_2\ \{G_{2^+}(1.9)\}_3\{G_{1^+}(2.6)G_{2^-}(2.8)G_{3^+}(2.9)\}_4$
P_3	$\{G_{1^-}(3.1)G_{3^+}(2.0)\}_2\ \{G_{1^-}(6.6)G_{3^+}(1.7)\}_3\{G_{1^-}(15)G_{2^-}(6.2)G_{3^+}(2.2)\}_4$

(a)

Gene	G_1	G_2	G_3
Score	0.8	0.6	0.1

(b)

III. DEFINITIONS AND PROBLEM STATEMENT

A. A Time course Microarray dataset and its transformation to a time course sequential dataset

A time course microarray dataset cannot be used directly to mine high utility gene regulation sequential patterns. In this section, we describe how to convert a time course microarray dataset to a proper *time course sequential dataset*.

Table I(a) shows an example of time course microarray dataset obtained from a biological investigation which consists of three patients whose IDs are P_1, P_2 and P_3. In this table, the gene expression values of three genes G_1, G_2 and G_3 are presented over four time point samples TS_1, TS_2, TS_3 and TS_4.

In each time sample, each gene has a *temporal behavior* which is expressed by a real value. We consider the first time sample as a baseline to derive the temporal behavior of each gene at each time sample. That is, the *temporal behavior* of a gene at a time sample *TS* is the expression value of the gene at *TS* divided by the expression value of the gene at the first time sample. It represents the degree of expression of the gene at time sample TS. Table I (b) shows the temporal behavior values as a fold change matrix.

Given the fold change matrix and a threshold γ, each expression value in the dataset is transformed as *up-regulated* (representing by $+$ meaning that the value is greater than γ), *down-regulated* (representing by $-$ meaning that the value is less than -γ), or *normal* (neither expressed nor repressed) and only the gene expressions that are up-regulated or down-regulated are preserved[2]. Each gene (i.e., G_x) in a sample can be thought of as being one of two $items$, one item referring to the gene being up (i.e., G_{x^+}), the other referring to the gene being down (i.e., G_{x^-}).

Given $\gamma = 1.5$, Table II(a) shows the converted dataset (i.e., the *time-course sequential* dataset). For example, in patient P_1, up-regulated $G_{1^+}(2.2)$ and down-regulated $G_{2^-}(3.2)$ are considered to occur at the same time (i.e., TS_2), where 2.2 and 3.2 are the temporal behavior of G_{1^+} and G_{2^-} (as defined above) respectively.

[2]This threshold is used to differentiate noisy behavior from important temporal behavior.

B. Definitions

Let $G = \{G_{1^+}, G_{1^-}, G_{2^+}, G_{2^-}, ..., G_{n^+}, G_{n^-}\}$ be a set of distinct gene regulation items. A *geneset* GS is a set of gene regulation items. A *time-course sequential* dataset is a set of patients $\{P_1, P_2, ..., P_K\}$, where each patient has a patient identifier P_r and consists of an ordered list of *time point samples (or in brief time samples (TSs))* where each TS is a geneset. The time sample TS_d for patient P_r is denoted as P_r^d.

Definition 1: The **importance of gene** g is a score which is calculated based on one or more disease-related variables $var_1, var_2, ..., var_k$ which is defined as follows. $GI(g) = f_g(var_1, var_2, ..., var_k)$, where f_g is the function for calculating the importance of g.

For example, Table II(b) shows the importance of genes with respect to a disease. In this work, the importance of G_x represents the importance of both G_{x^+} and G_{x^-} gene items.

Definition 2: **Internal utility** or *temporal behavior* of a gene g is a real value assigned to g in the time sample TS_d of patient P_r (i.e., P_r^d). It is denoted as $IGU_{dis}(g, P_r^d)$ and is defined as the expression value of g at TS_d divided by the expression value of g at the first time sample in P_r.

For example, in Table II(a), given gene G_{1^-} and time sample TS_3 in sequence P_1, $IGU(G_{1^-}, P_1^3) = 2.4$. This value specifies the relative abundance of the gene in the time sample.

Definition 3: (**Utility of gene** g **in time sample** P_r^d) Given gene g and time sample P_r^d, *gene utility* is defined as a combination of gene importance and internal utility of g w.r.t. disease dis as follows. $GU(g, P_r^d) = f_{gu}(GI(g), IGU(g, P_r^d))$, where f_{gu} is the function for calculating utility.
For simplicity, we define the f_{gu} function as $f_{gu}(GI(g), IGU(g, P_r^d)) = GI(g) \cdot IGU(g, P_r^d)$.

Definition 4: The **utility of a geneset** GS **in a time sample** TS_d **of a patient** P_r where $GS \subseteq TS_d$, is defined as $GU(GS, P_r^d) = \sum_{g \in GS} GU(g, P_r^d)$.

Definition 5: (**Occurrence of a sequence** α **in a patient** P_r) Given a patient $P_r = \langle P_r^1, P_r^2, ..., P_r^n \rangle$ and a gene regulation sequence $\alpha = \langle GS_1, GS_2, ..., GS_Z \rangle$ where P_r^i is a time sample and GS_i is a geneset, α occurs in P_r iff there exist integers $1 \leq e_1 < e_2 < ... < e_Z \leq n$ such that

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.

$GS_1 \subseteq P_r^{e_1}, GS_2 \subseteq P_r^{e_2}, ..., GS_Z \subseteq P_r^{e_Z}$. The ordered list of genesets $\langle P_r^{e_1}, P_r^{e_2}, ..., P_r^{e_Z} \rangle$ is called an *occurrence of* α *in* P_r. The set of all occurrences of α in P_r is denoted as $OccSet(\alpha, P_r)$.

Definition 6: The **(utility of a gene regulation sequential pattern** α **in a patient sequence** P_r**)** Let $\tilde{o} = \langle P_r^{e_1}, P_r^{e_2}, ..., P_r^{e_Z} \rangle$ be an occurrence of $\alpha = \langle GS_1, GS_2, ..., GS_Z \rangle$ in the sequence P_r. The utility of α w.r.t. $\tilde{o}$ is defined as $GU(\alpha, \tilde{o}) = \sum_{i=1}^{Z} GU(GS_i, P_r^{e_i})$. The utility of α in P_r is defined as $GU(\alpha, P_r) = \max\{GU(\alpha, \tilde{o}) \mid \tilde{o} \in OccSet(\alpha, P_r)\}$.

Definition 7: The **(utility of a gene regulation sequence** α **in a time course sequential dataset** D**)** The utility of a gene regulation sequence α in a time course sequential dataset D is defined as $GU(\alpha, D) = \sum_{P_r \in D} GU(\alpha, P_r)$.

Definition 8: **(High Utility Gene regulation Sequence (HUGS))** Given a threshold δ, a sequence α is a *High Utility Gene Regulation Sequence* (HUGS) in a time course sequential dataset D, iff $GU(\alpha, D)$ is no less than δ.

Definition 9: **(Top-k High Utility Gene regulation Sequence in a time course sequential dataset** D**)** A gene regulation sequence α is called a top-k High Utility Gene Regulation Sequence (*HUGS*) in D, if there are less than k sequences whose utility value in D is no less than $GU(\alpha, D)$.

Problem Statement. Given a time course sequential dataset D and a user-defined number k, the problem of finding the complete set of top-k high utility gene regulation sequential patterns in D is to discover all the gene regulation sequential patterns whose utility is no less than $minUtil_{opt}$, where $minUtil_{opt} = \min\{GU(\beta, D) | \beta \in THUGS_D\}$, where $THUGS_D$ is the set of top-k HUGSs over D.

IV. Top-k Utility-based Gene Regulation Sequential Pattern Discovery

In this section, we propose an efficient algorithm called *TU-SEQ (Top-k Utility-based gene regulation SEQuential pattern discovery)* to find top-k *HUGSs* without specifying the minimum threshold. First, a basic approach called *TU-SEQ*$_{Base}$ is presented. Later, we present a novel strategy for initializing the threshold with respect to the given k in *TU-SEQ*$_{Base}$.

A. TU-SEQ$_{Base}$ approach

The proposed baseline approach *TU-SEQ*$_{Base}$ takes k as an input parameter and returns top-k sequences with the highest utilities in a time course sequential dataset D. It is an extension of *HUSP-Stream*, our recent proposed method for mining high utility sequential patterns [14], and it applies the idea of *ItemUtilLists* and *HUSP-Tree* to maintain the information of potential top-k HUGSs. *HUSP-Stream* is a threshold-based approach and is not able to discover top-k HUGSs.

We first briefly describe *ItmeUtilLists* and *HUSP-Tree*. For more details about the data structures, readers can refer to [14].

ItemUtilLists is a vertical representation of the time samples in the dataset. The *ItemUtilLists* of a gene G consists of several tuples. Each tuple stores the utility of gene G in the time sample P_v^u (i.e., time sample TS_u in patient P_v) that contains G. Each tuple has three fields: PID, TID and $util$. Fields PID and TID store the identifiers of P_v and TS_u, respectively. Field $util$ stores the utility of G in P_v^u (Definition 3). Figure 1(a) shows the *ItemUtilLists* of G_{1^+}, G_{2^-} and G_{3^-} in Table II(a).

A **HUSP-Tree** is a lexicographic sequence tree where each non-root node represents a sequence of genesets. Figure 1 (b) shows part of the *HUSP-Tree* for the the dataset in Table II (a), where the root is empty. Each node at the first level under the root represents a sequence of length 1, a node on the second level represents a 2-sequence, and so on. Each non-root node of a *HUSP-Tree* is designed to have a field, called *SeqUtilList*, for maintaining information about the sequence represented by a node. The *sequence utility list (SeqUtilList)* of a sequence α is a list of three-value tuples. Each tuple $\langle PID, TID, util \rangle$ represents an occurrence of α in a sequence of the dataset and the utility of α with respect to the occurrence. The PID in a tuple is the ID of the patient in which α occurs, TID is the ID of the last time sample in the occurrence of α, and $util$ is the utility value of α with respect to the occurrence. We denote the $SeqUtilList$ of α as $SeqUtilList(\alpha)$.

A non-root node in a *HUSP-Tree* is either *I-node* or *S-node*.

Definition 10: **(I-concatenate Sequence)** Given a sequence pattern α, an *I-concatenate* pattern β represents a sequence generated by adding a gene G into the last geneset of α (denoted as $\alpha \oplus G$). A node whose pattern is an I-concatenate sequence is called *I-node*.

Definition 11: **(S-concatenate Sequence)** Given a sequence α, an *S-concatenate* pattern β represents a sequence generated by adding a geneset $\{G\}$ after the last geneset of α (denoted as $\alpha \otimes G$). A node whose pattern is a S-concatenate sequence is called *S-node*.

In Figure 1(b), the node for sequence $\{G_{1^+}G_{3^+}\}$ is an *I-node*, while the node for $\{G_{1^+}\}\{G_{3^+}\}$ is a *S-node*.

HUSP-Tree Construction: *HUSP-Tree* is constructed recursively in a top-down fashion using *ItemUtilLists*. The first level of the tree under the root is constructed by using the genes in *ItemUtilLists* as nodes. The *SeqUtilList* of these nodes is the *ItemUtilList* of the items. Given a non-root node, its child nodes are generated using *I-Step* and *S-Step*, which generate *I-nodes* and *S-nodes* respectively. We demonstrate *I-Step* and *S-Step* procedures of pattern $\alpha = \{G_{1^+}\}$ with sequence P_2 in Table II (a). We start from the *I-Step*. Given the pattern α and gene $G = G_{2^+}$, in order to form $\beta = \{G_{1^+}G_{2^+}\}$ and calculate its utility, *I-Step* is applied as follows. According to Table II (a), only time sample P_2^2 has G_{2^+} can be used to form sequence β. The utility of β is $GU(\alpha, P_2^2)$ plus the newly added gene's utility which is $GU(G_{2^+}, P_2^2)$. Therefore, $GU(\beta, P_2) = 6.1 \times 0.8 + 3.2 \times 0.6 = 4.88 + 1.92 = 6.8$. Given pattern $\alpha = \{G_{1^+}G_{2^+}\}$ and $G = G_{3^+}$, to construct pattern $\beta = \{G_{1^+}G_{2^+}\}\{G_{3^+}\}$ and calculate its utility, *S-Step* works as follows. Since geneset $\{G_{3^+}\}$ must occur in any

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.

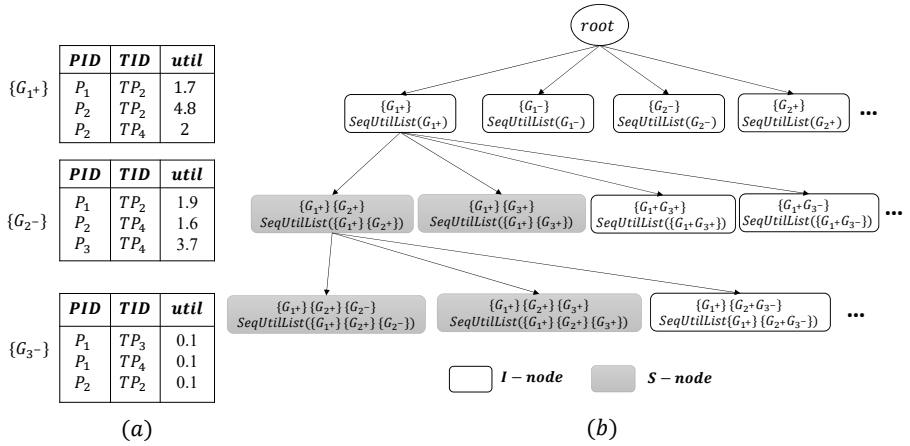


Fig. 1. (a) ItemUtilLists of G_{1+}, G_{2-} and G_{3-}, (b) An example of HUSP-Tree for the dataset in Table II(a)

time samples after α occurs, the only case for $\{G_{3+}\}$ is in P_2^4. Hence, $GU(\beta, P_2) = \{6.8 + 0.2\} = 7$.

In addition to *ItemUtilLists* and *HUSP-Tree*, *T-HUSP*$_{Base}$ engages a structure called *TKList* to maintain the information of top-k high utility gene regulation sequential patterns.

Definition 12: **Top-k HUGS List (TKList)** is a fixed-size sorted list which maintains the top-k high utility gene regulation sequential patterns and their *utility* values. Each tuple in *TKList* has two elements: $\langle \alpha, util \rangle$, where α is the pattern and $util$ is the utility of pattern α in the dataset.

Since the threshold is not given as an input parameter, *TU-SEQ*$_{Base}$ employs a variable called $minUtil$ which is the current threshold and is set to zero at the beginning. This variable is used to prune unpromising candidates during the mining process.

Given a time course sequential dataset D and k, TU-SEQ$_{Base}$ finds top-k HUGSs as follows. TU-SEQ$_{Base}$ first sets $minUtil$ to 0. Then, it constructs *ItemUtilList* and *HUSP-Tree* by applying the *S-Step* and *I-Step* procedures. As soon as a new node is added to *HUSP-Tree*, the pattern represented by the node and its *utility* are added as a new tuple to $TKList$. Once k valid patterns are found, the $minUtil$ is raised to the $util$ value of the pattern with the lowest *util* value in $TKList$. Raising the $minUtil$ value is used to prune the search space when searching for more patterns. Thereafter, whenever a new node is inserted to the tree, its pattern is added to $TKList$. Then, the patterns in $TKList$ whose *util* is less than $minUtil$ are removed from $TKList$, and $minUtil$ is updated by the *util* value of the *kth* pattern in $TKList$. TU-SEQ$_{Base}$ continues constructing *HUSP-Tree* and finding more patterns until no node can be generated, which means that it has found the top-k *HUGSs* in the dataset.

Since *HUSP-Stream* is correct and complete [14], it is clear that *TU-SEQ*$_{Base}$ is correct and will not miss any top-k *HUGSs*.

B. PES (Pre-Evaluation using genes and sequences) Strategy

Although TU-SEQ$_{Base}$ correctly discovers the top-k high utility gene regulation sequential patterns in the dataset, it generates too many invalid sequence candidates since $minUtil$ starts from 0. This directly degrades the performance of the mining task. To address this problem, we propose an effective strategy for initializing the threshold before *HUSP-Tree* construction to improve the performance. The development of the proposed strategy is based on the following lemmas.

Lemma 1: Given a time course sequential dataset D, let L = $\{\alpha_1, \alpha_2, ..., \alpha_m\}$ be a set of gene regulation sequences ($m \geq k$), where α_i is the sequence with the i-th highest utility value in L. For any sequence β, if $GU(\beta, D) < GU(\alpha_k, D)$, β is not a top-k high utility gene regulation sequence.

Rationale. According to Definition 9, if there exist k sequences with utility values higher than the utility of β, β is not a top-k high utility gene regulation sequential pattern.

Lemma 2: Let $L = \langle \alpha_1, \alpha_2, ..., \alpha_m \rangle$ be a set of sequences ($m \geq k$), where α_i is the i-th sequence in L, $\forall i < j, GU(\alpha_i, D) \geq GU(\alpha_j, D)$ and H_δ be the set of high utility gene regulation sequential patterns when the threshold is δ. If $minUtil = GU(\alpha_k)$, then $H_{minUtil_{opt}} \subseteq H_{minUtil}$.

Rationale. Let H be the complete set of top-k high utility gene regulation sequential patterns. If $|H| \geq k$, $minUtil_{opt} = \min\{GU(\alpha, D) | \alpha \in H\}$. Since $minUtil_{opt} = min\{GU(\alpha, D) | \alpha \in H\} \geq \min\{GU(\alpha_i) | \alpha_i \in L, 1 \leq i \leq k\} = GU(\alpha_k, D) = minUtil$, then $minUtil_{opt} \geq minUtil$ and $H_{minUtil_{opt}} \subseteq H_{minUtil}$.

According to the above lemmas, *PES* initializes *TKList* by inserting the *utility* of genes and sequences in the dataset to the *TKList* before the tree construction. After all time samples in the dataset D are successfully inserted to $ItemUtilList$, *PES* calculates the *utility* of each gene and each sequence. Given the updated *TKList*, $minUtil$ is initialized by the *util* value of kth pattern in *TKList*.

Example 1: Given $k = 4$, the time course sequential dataset D in Table II(a), the *utility* of gene G_{1+} in D is calculated as follows: $GU(G_{1+}, D) = GU(G_{1+}, P_1) + GU(G_{1+}, P_2) + GU(G_{1+}, P_3) = 1.76 + 4.88 + 0 = 6.64$. The *utility* values of other genes in D can be calculated similarly, $GU(G_{1-}, D) = 15.84$, $GU(G_{2+}, D) = 3.72$, $GU(G_{2-}, D) =$

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.

Algorithm 1 *TU-SEQ*

Input: a time-course sequential dataset D, k
Output: $THUGS_D$

1: $ItemUtilLists, TKList \leftarrow \emptyset$
2: **for** each time sample $P_r^i \in D$ **do**
3: **for** each gene $G \in P_r^i$ **do**
4: insert $\langle r, i, GU(G, P_r^i)\rangle$ to $ItemUtilLists(G)$
5: **end for**
6: **end for**
7: Initialize $TKList$ and $minUtil$ using **PES strategy**.
8: Construct *HUSP-Tree* using $ItemUtilLists$ and $minUtil$
9: Update $minUtil$ whenever a new node is added to the tree
10: **if** the user requests to get top-k HUGSs **then**
11: $THUGS_D \leftarrow$ all the patterns and their $util$ values stored in $TKList$
12: **end if**
13: **Return** $THUGS_D$ if requested

7.32, $GU(G_{3^+}, D) = 0.51$ and $GU(G_{3^-}, D) = 0.35$. The *utility* of each sequence can be easily calculated using *ItemUtilLists*. After D is processed, P_1 and its *utility* (e.g., 11.5) is inserted into the $TKList$. Similarly, the other sequences in D (e.g., P_2 (12.18) and P_3(25.07)) are scanned and then they are inserted into the $TKList$. With the three sequences, six genes and their *utility* values in D, the *util* values in the *TKList* are $\{25.7, 15.84, 12.18, 11.5\}$. Hence, $minUtil = 11.5$ after applying *PES* strategy.

As seen from the example, the *PES* strategy effectively raises the minimum threshold to a reasonable level before the tree construction, and prevents from generating unpromising candidates.

C. Overview of TU-SEQ

The overview of *TU-SEQ* is presented in Algorithm 1. Given a time course sequential dataset D, *TU-SEQ* first constructs the *ItemUtilLists* for storing the information for every gene in each time sample in D. Then, it initializes $TKList$ and $minUtil$ by applying *PES* strategy based on genes in the $ItemUtilLists$ and the sequences in the dataset. Then, *TU-SEQ* constructs *HUSP-Tree* using *I-Step* and *S-Step*. During the tree construction, whenever a new node is added to the tree, $TKList$ and $minUtil$ are updated as explained in section IV-A. Finally, if the user requests to find top-k *HUGSs* from the dataset, *TU-SEQ* returns all the patterns and their $util$ values in the $TKList$ as top-k *HUGSs* (i.e., $THUGS_D$).

V. Experimental Results

In this section, the proposed method for finding top-k high utility gene regulation sequential patterns is evaluated. All the algorithms are implemented in Java. The experiments are conducted on an Intel(R) Core(TM) i7 2.80 GHz computer with 12 GB of RAM. The *GSE6377* dataset [16], downloaded from the *GEMMA database*[3], is used in our experiments. McDunn et al. [16] attempted to detect 8,793 transcriptional changes in 11 ventilator-associated pneumonia patients leukocytes across 10 time samples.

[3]http://www.chibi.ubc.ca/Gemma/home.html

A. The importance of genes with respect to pneumonia

Several databases have been developed providing associations between genes and diseases such as *CTD* [17]. Each of these resources considers different aspects of the phenotype-genotype relationship and they are not complete. Based on our investigation, *DisGeNET*[4] is a discovery platform which integrates different databases with information extracted from the literature to create a comprehensive view of the state of the art knowledge within this research field. In this paper, we consider the *score* proposed by *DisGeNET*[5] as the importance of each gene with respect to the disease. This score considers several variables such as number and type of sources (level of curation, model organisms) and the number of publications supporting the association to rank genes with respect to a specific disease. Table III shows top-20 genes w.r.t. *Pneumonia* and their scores.

We calculate the utility[6] of gene G in time sample P_r^d as follows: $GU(G, P_r^d) = GI(G) \times IGU(G, P_r^d)$, where $GI(G)$ is the importance of G w.r.t. *Pneumonia* retrieved from $DisGeNET$ and $IGU(G, P_r^d)$ is the expression value of G in time sample TS_d in sequence P_r.

B. HUGSs comparison with FGSs

In this section, we address whether patterns discovered by *TU-SEQ* contain potential genes/regulations which have not been reported in previous literature yet. We first run *TU-SEQ* to extract top-k *HUGSs* with respect to *Pneumonia*. We also run a recent method called *CTGR-Span* [2], to discover frequent gene regulation sequential patterns (i.e., *FGSs*) from the dataset. Given a gene regulation sequential pattern α and a disease dis, we evaluate the quality of the results using *popularity of a sequence* [18] which is defined as follows $Pop(\alpha, dis) = \frac{\sum_{i \in \alpha} w(i,dis)}{|\alpha|}$, where $w(i, dis)$ is the importance of the popular gene i for disease dis. Without loss of generality, we consider the genes presented in Table III as popular genes and $w(i, dis) = 20 - rank(i, dis) + 1$. For the genes which are not presented in the list, $w(i, dis) = 1$.

Table IV shows top-4 *HUGSs* extracted by *TU-SEQ* and top-4 *FGSs* extracted by *CTGR-Span*, sorted by the utility and support respectively. Table IV suggests that the frequent sequences are not necessarily popular w.r.t. the disease even though their support value is high. This is due to the fact that these patterns are discovered based on their frequency in the dataset which is not informative enough. On the other hand, *TU-SEQ* returns the patterns whose popularity is relatively high. These patterns help biologists select relevant sequences regarding a specific disease and also identify the relationships between important genes and the other genes.

Table V shows the average value of utility (i.e., *GU*), *Pop* and *Sup* for top-1000 patterns returned by the methods. Given sequence α, the last two columns present harmonic mean of

[4]http://www.disgenet.org/web/DisGeNET/menu
[5]http://www.disgenet.org/web/DisGeNET/menu
[6]The model can be plugged in as desired. The use of more sophisticated the model may further improve the quality of the results.

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.

TABLE III
TOP-20 GENES RELATED TO PNEUMONIA

Rank	*Gene*	*GI(Gene)*	*Rank*	*Gene*	*GI(Gene)*	*Rank*	*Gene*	*GI(Gene)*	*Rank*	*Gene*	*GI(Gene)*
1	*CAT*	100.00	6	*SFTPC*	100.00	11	*SFTPA1*	100.00	16	*HMGB1*	90.37
2	*PDPN*	100.00	7	*SFTPB*	100.00	12	*CYP2J2*	100.00	17	*CR1*	90.34
3	*TLR6*	100.00	8	*PECAM1*	100.00	13	*F2*	100.00	18	*MASP2*	90.30
4	*TLR2*	100.00	9	*ITGB3*	100.00	14	*CXCL1*	100.00	19	*FCGR2A*	90.30
5	*SFTPD*	100.00	10	*CXCL2*	100.00	15	*MBL2*	90.89	20	*IL17A*	90.07

TABLE IV
TOP-4 HUGSS VERSUS TOP-4 FGSS WITH RESPECT TO SUPPORT AND GDA

Algorithm	*ID.*	*Sequence of genes(e.g.,α)*	*Support*	*Utility*
$TU-SEQ$	$HUGS_1$	(*CAT*) (*CAT MBL2*) (*CAT*)	9	**250600**
	$HUGS_2$	(*GOLPH3 PDPN*) (*CAT*) (*PDPN*) (*CAT*) (*PDPN*)	9	**250325**
	$HUGS_3$	(*CAT MBL2*) (*CAT*) (*CAT*)	9	**249741**
	$HUGS_4$	(*PDPN*) (*CAT*) (*PDPN*) (*CAT*) (*PDPN*)	9	**243037**
$CTGR-Span$	FGS_1	(*LCN2 S100A12*) (*LCN2*)	**11**	59981
	FGS_2	(*LCN2*) (*S100A12*) (*CSF3 LCN2*)	**11**	59962
	FGS_3	(*CSF3 S100A12*)	**11**	59931
	FGS_4	(*LCN2 S100A12*) (*LCN2 S100A12*)	**11**	58514

TABLE V
THE AVERAGE VALUE OF *Sup*, *GU*, *Pop*, *GU-Pop* AND *Sup-Pop* FOR TOP-1000 SEQUENCES RETURNED BY THE METHODS

Method	Sup	GU	Pop	GU-Pop	Sup-Pop
TU-SEQ	5	**198939**	**12.5**	**24.96**	**7.32**
CTGR-Span	**10**	44691	1.02	2.05	1.86

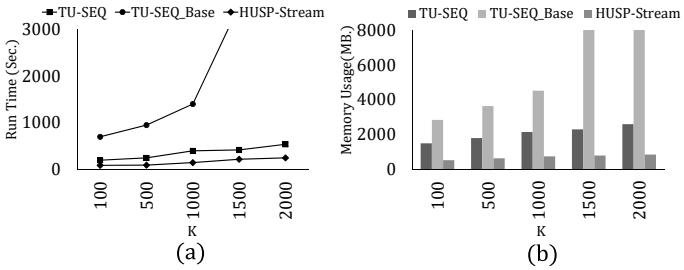


Fig. 2. (a) Run time, (b) Memory usage on the GSE3677 Dataset

(GU, Pop) and *(Sup, Pop)* which are calculated as follows: $GU - Pop = 2 \times \frac{GU \times Pop}{GU + Pop}$, $Sup - Pop = 2 \times \frac{Sup \times Pop}{Sup + Pop}$. According to Table V, the higher values of these measures for *TU-SEQ* show that even though the patterns returned by *TU-SEQ* are not as frequent as those of returned by *CTGR-Span*, they are not only much more relevant to the disease, but also they are frequent enough.

C. Efficiency of TU-SEQ

In this section, we evaluate the performance of the algorithms using the following measures: (1) *Run Time (sec.)*: the total execution time of the algorithms. and (2) *Memory Usage (MB)*: the average memory consumption per window.

Since there is no known algorithm can solve the problem of mining *top-k utility-based gene regulation sequential patterns*, we thus compare *TU-SEQ* with our proposed baseline approach (i.e., *TU-SEQ*$_{Base}$) as described in subsection IV-A. We also use the threshold-based approach (i.e., *HUSP-Stream*) proposed in [14] as another baseline approach. After getting the *utility* of the k-th pattern, that is the optimal minimum threshold in Definition 9, we use this value as the threshold for running the threshold-based method.

We compare *TU-SEQ* with TU-SEQ$_{Base}$ and *HUSP-Stream* on the *GSE6377* dataset. The run time of mining top-k high utility gene regulation sequential patterns by the methods is presented in Figure 2(a). The results show that *TU-SEQ* is more than 5 times faster than *TU-SEQ*$_{Base}$. For larger values of k, *TU-SEQ*$_{Base}$ cannot finish the mining in 12+ hours. Besides, the gap between *TU-SEQ* and *TU-SEQ*$_{Base}$ increases with the increase of k. The results indicate that the proposed strategy (i.e., *PES* strategy) is effective for top-k pattern mining.

The memory consumption of the algorithms on the dataset is shown in Figure 2(b). It can be seen that *TU-SEQ* uses less memory than *TU-SEQ*$_{Base}$. The reason is that *TU-SEQ* creates a smaller search space because it applies the proposed strategy, thus increases the threshold quicker than *TU-SEQ*$_{Base}$. Since all the methods use similar approach to construct the tree, the main factor in memory consumption is the threshold used by each of them. *HUSP-Stream* uses the optimal threshold (i.e., $minUtil_{opt}$), hence it prunes the search space efficiently and its memory usage is less than the other methods.

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.

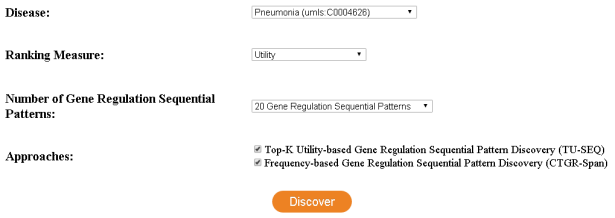


Fig. 3. First page of the system with parameters

D. Demonstration

We also develop a web interface[7] to our system using Java. To the best of our knowledge, this is the first demonstration for *top-k high utility gene regulation sequential pattern discovery*. In order to evaluate *TU-SEQ* to find top-k *HUGSs* from a time course gene sequential dataset, we mine the *GSE6377* dataset. According to *DisGNET*, *Athma* and *Rheumatoid Arthritis* are among top 10 diseases that share genes with *Pneumonia*. Hence, in our demonstration, we also present top-k high utility gene regulation sequential patterns with respect to *Athma* and *Rheumatoid Arthritis*. Moreover, the patterns discovered by *CTGR-Span* [2] are presented. In the first page of the interface, the user can specify *disease*, *ranking measure*, number of output gene regulation sequences (i.e., k) and *discovery method(s)*.

In the demonstration, users are able to compare the algorithms in the following aspects:

1) *Meaningful results:* Our method based on the utility model produces more meaningful sequences than the other method.
2) *Top-k gene regulation sequential patterns presentation:* The sequences retrieved by the methods are provided in a meaningful graphical presentation.
3) *Additional information:* Additional information such as values for the other measures than the selected one for ranking and top-20 genes related to the selected disease.

VI. Conclusion

In this paper, we defined the problem of *top-k utility-based gene regulation sequential pattern discovery* to find patterns with stronger meanings in biology. By solving this problem, we addressed the limitations of previous frequency-based gene regulation sequential pattern mining methods. We first proposed a *utility* model by considering the importance of genes with respect to a disease and their temporal behavior. Then, using the utility model, we proposed an efficient algorithm called *TU-SEQ* to find top-k high utility gene regulation sequential patterns. Our experiments suggested that *TU-SEQ* is much more efficient and scalable than baseline algorithms for top-k high utility gene sequential pattern discovery. We also showed that *TU-SEQ* is an effective tools to provide biologists with further insights into the relationships of gene regulatory events and interactions in biological studies with respect to a specific disease.

[7]http://graph.cse.yorku.ca:8080/GeneAssociation/

VII. Acknowledgment

This work is funded in part by Natural Sciences and Engineering Research Council of Canada (NSERC), and the Big Data Research, Analytics, and Information Network (BRAIN) Alliance established by the Ontario Research Fund - Research Excellence Program (ORF-RE). The authors would like to thank IBM Platform Computing for their collaboration in our joint NSERC CRD project.

References

[1] J. N. Hirschhorn and M. J. Daly, "Genome-wide association studies for common diseases and complex traits," *Nature Reviews Genetics*, vol. 6, no. 2, pp. 95–108, 2005.
[2] C.-P. Cheng, Y.-C. Liu, Y.-L. Tsai, and V. S. Tseng, "An efficient method for mining cross-timepoint gene regulation sequential patterns from time course gene expression datasets," *BMC Bioinformatics*, vol. 14, no. 12, pp. 1–12, 2013.
[3] S. Bringay, M. Roche, M. Teisseire, P. Poncelet, R. A. Rassoul, J.-M. Verdier, and G. Devau, "Discovering novelty in sequential patterns: application for analysis of microarray data on alzheimer disease," in *MedInfo: Congress on Medical Informatics*, vol. 160, no. Pt 2. Stud Health Technol Inform, 2010, pp. 1314–1318.
[4] E. Georgii, L. Richter, U. Rückert, and S. Kramer, "Analyzing microarray data using quantitative association rules," *Bioinformatics*, vol. 21, no. suppl 2, pp. ii123–ii129, 2005.
[5] C. Mooney and J. Roddick, "Sequential pattern mining approaches and algorithms," *ACM Comput. Surv.*, vol. 45, no. 2, pp. 19:1–19:39, 2013.
[6] C. Creighton and S. Hanash, "Mining gene expression databases for association rules," *Bioinformatics*, vol. 19, no. 1, pp. 79–86, 2003.
[7] Q. Chen and Y.-P. P. Chen, "Mining frequent patterns for amp-activated protein kinase regulation on skeletal muscle," *BMC bioinformatics*, vol. 7, no. 1, p. 1, 2006.
[8] C.-M. Hsu, C.-Y. Chen, C.-C. Hsu, and B.-J. Liu, "Efficient discovery of structural motifs from protein sequences with combination of flexible intra-and inter-block gap constraints," in *Pacific-Asia Conference on Knowledge Discovery and Data Mining*. Springer, 2006, pp. 530–539.
[9] C. F. Ahmed, S. K. Tanbeer, and B. Jeong, "A novel approach for mining high-utility sequential patterns in sequence databases," *In ETRI Journal*, vol. 32, pp. 676–686, 2010.
[10] B. Shie, H. Hsiao, and V. S. Tseng, "Efficient algorithms for discovering high utility user behavior patterns in mobile commerce environments," *In KAIS journal*, vol. 37, 2013.
[11] C. F. Ahmed, S. Tanbeer, and B. Jeong, "A framework for mining high utility web access sequences," *In IETE Journal*, vol. 28, pp. 3–16, 2011.
[12] J. Yin, Z. Zheng, and L. Cao, "Uspan: An efficient algorithm for mining high utility sequential patterns," in *In Proc. of ACM SIGKDD*, 2012, pp. 660–668.
[13] O. K. Alkan and P. Karagoz, "Crom and huspext: Improving efficiency of high utility sequential pattern extraction," *IEEE Transactions on Knowledge and Data Engineering*, vol. 27, no. 10, pp. 2645–2657, Oct 2015.
[14] M. Zihayat, C.-W. Wu, A. An, and V. S. Tseng, "Mining high utility sequential patterns from evolving data streams," in *ASE BD&SI '15*, 2015, pp. 52:1–52:6.
[15] J. Pei, J. Han, B. Mortazavi-Asl, Q. Chen, U. Dayal, and M. Hsu, "Mining sequential patterns by pattern-growth: The prefixspan approach," *TKDE*, vol. 16, pp. 1424–1440, 2004.
[16] J. McDunn, K. Husain, A. Polpitiya, A. Burykin, Q. Li, W. Schierding, N. Lin, D. Dixon, and W. Zhang, "Plasticity of the systemic inflammatory response to acute infection during critical illness: development of the riboleukogram," *PloS one*, vol. 3, no. 2, p. e1564, 2008.
[17] A. P. Davis, C. G. Murphy, R. Johnson, J. M. Lay, K. Lennon-Hopkins, C. Saraceni-Richards, D. Sciaky, B. L. King, M. C. Rosenstein, T. C. Wiegers *et al.*, "The comparative toxicogenomics database: update 2013," *Nucleic acids research*, vol. 41, no. D1, pp. D1104–D1114, 2013.
[18] S. Bringay, "Discovering novelty in sequential patterns: application for analysis of microarray data on alzheimer disease," in *Studies in health technology and informatics*, 2010, pp. 1314–1318.

Authorized licensed use limited to: Ontario Tech University. Downloaded on November 10,2026 at 19:40:50 UTC from IEEE Xplore. Restrictions apply.